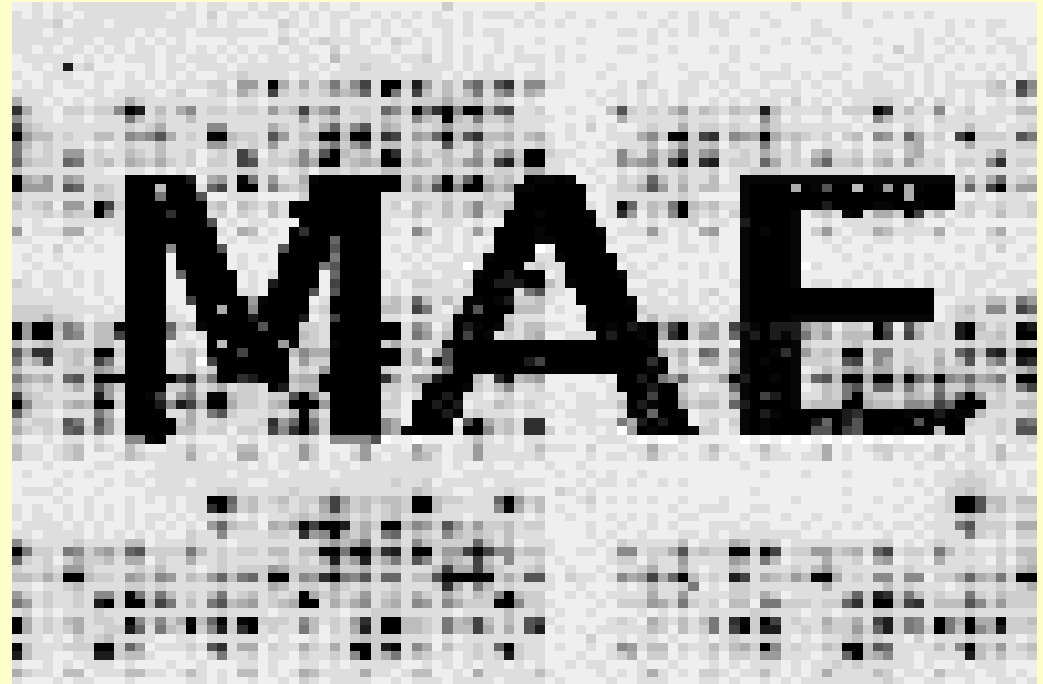


# II. Examples of MicroArray Explorer

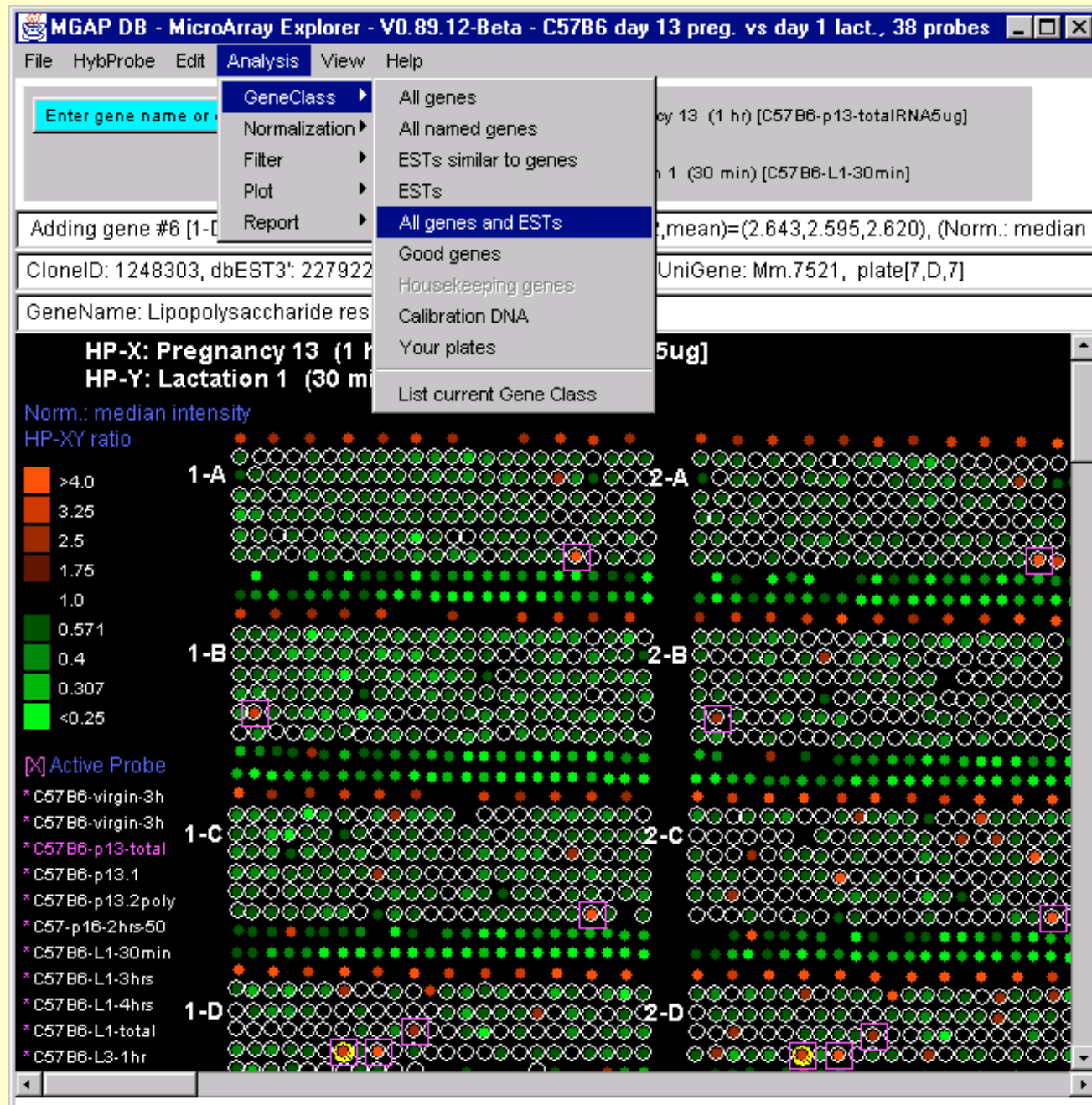


## Outline

1. Description
2. Importing data
3. Examples of analysis capabilities

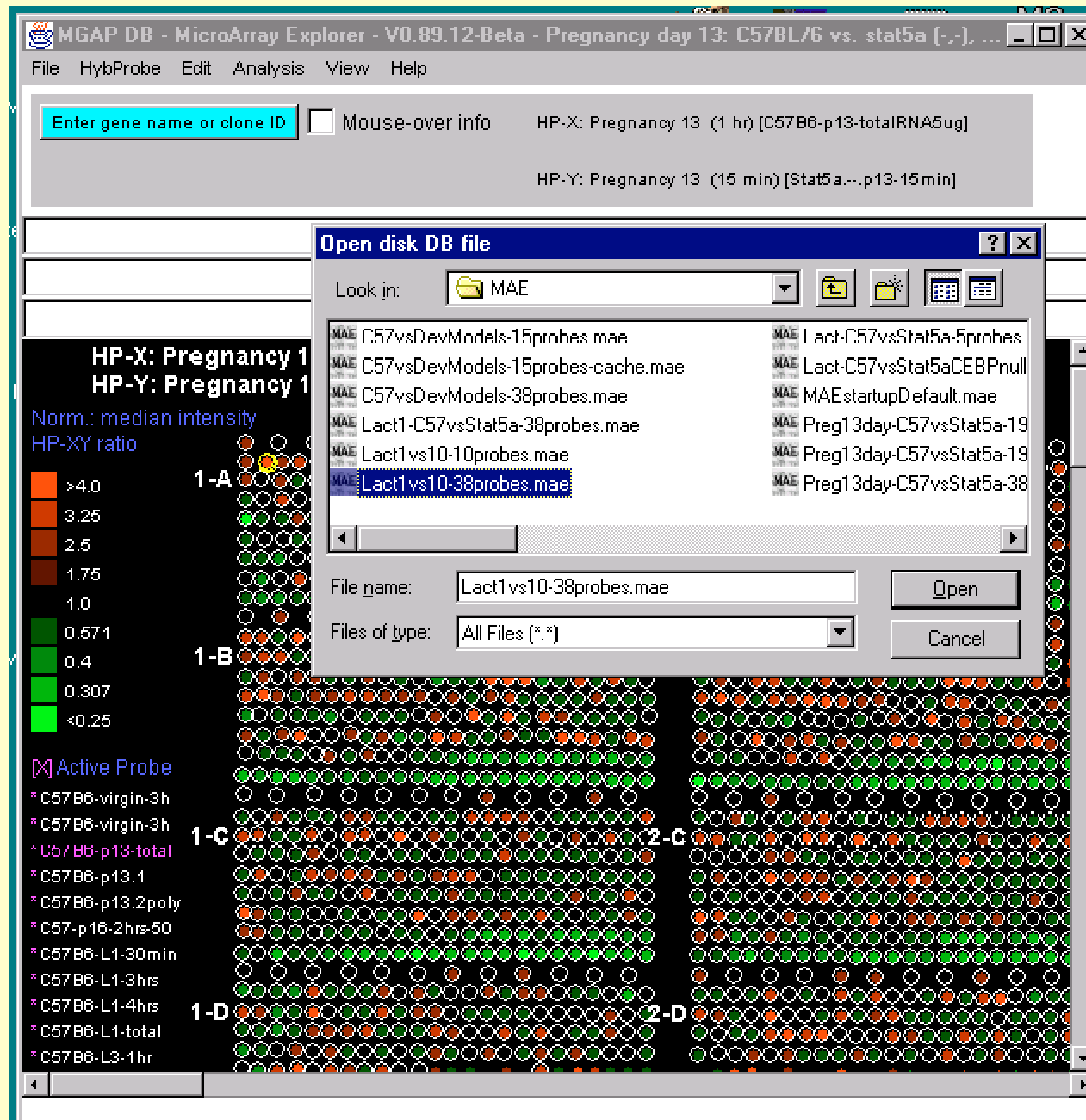
# II.1 MAExplorer uses GUI-based User Interface

- Specify sets of genes for *all named genes* and *all ESTs* indicated by white circles.



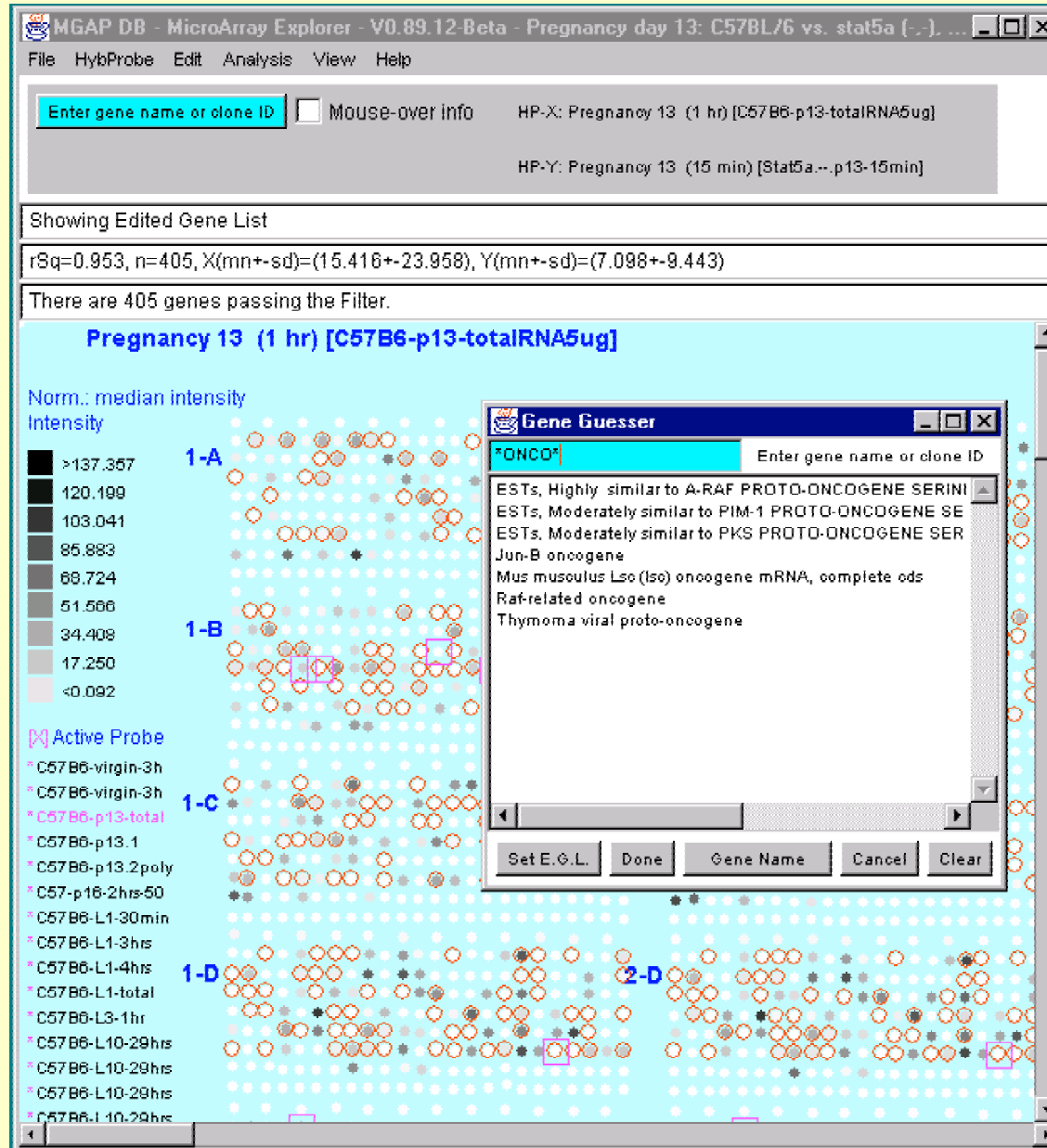
## II.2 Opening a Database from Local Disk

- In stand-alone mode, you may browse a project database containing startup databases.

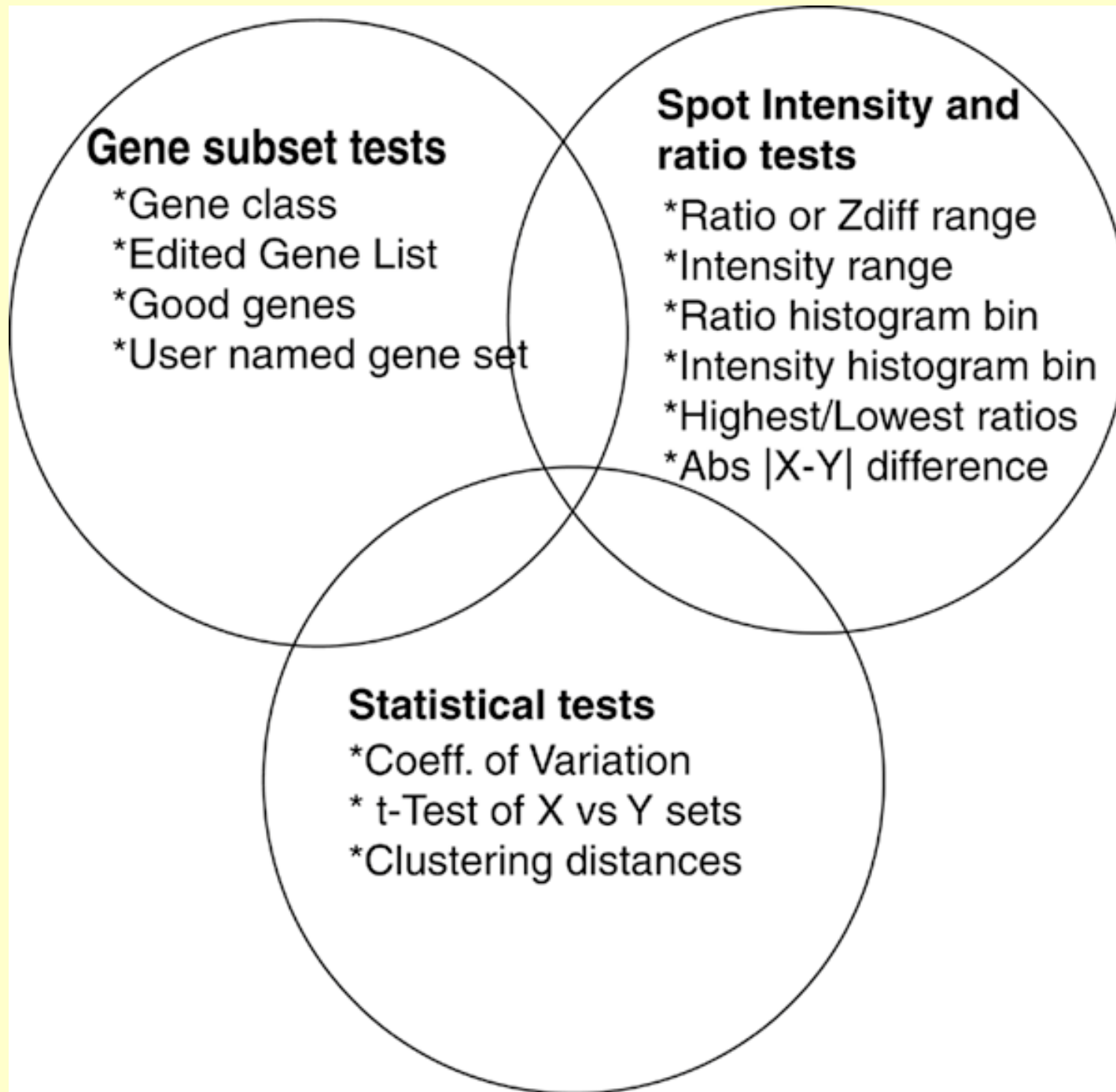


## II.3 Specify Gene or Gene Subset by Name

- Specify gene or gene subset by gene name guesser using wildcard sub-strings eg. “\*ONCO\*” indicated by magenta boxes in pseudo image - saved in ‘Edited Gene List’.



## II.4 Gene Data Filter is Intersection of Tests



# II.5 MAExplorer Data Filter Menu

The screenshot displays the MAExplorer software interface, version V0.89.35-Beta. The main window is titled "MGAP DB - MicroArray Explorer - V0.89.35-Beta - C57B6 day 13 preg. vs day 1 lact., ...". The menu bar includes File, HybProbe, Edit, Analysis, View, and Help. The Analysis menu is open, showing options like GeneClass, Normalization, Filter, Plot, and Report. The Filter menu is further expanded, listing various filtering criteria such as "Filter by GeneClass membership", "Filter by 'User Filter Gene Set' membership", "Filter by 'Edited Gene List' membership", "Filter by 'good genes list' membership", "Filter by genes with replicates", "Filter by ratio histogram bin", "Filter by intensity histogram bin", "Filter by spot intensity [S1:I2] sliders", "Filter by intensity [I1:I2] sliders", "Filter by ratio or Zdiff sliders", "Filter by Spot CV", "Filter by HP-X,HP-Y t-Test [p-Value] slider", "Filter by HP-X,HP-Y 'sets' t-Test [p-Value] slider", "Filter by HP-E clustering [Cluster Dist] slider", "Filter by Diff(HP-X,HP-Y) [Abs.Diff.] slider", "Filter genes with highest X/Y ratio or X-Y Zdiff", and "Filter genes with lowest X/Y ratio or X-Y Zdiff". The "Filter by ratio or Zdiff sliders" option is selected, and a sub-menu is open showing "Use ratio [R1:R2] or Zdiff [Z1:Z2] sliders" and "Outside range".

On the left side of the main window, there is a section titled "HP-X: C57B6 pregnancy" and "HP-Y: C57B6 lactation day 1". Below this, a color scale legend indicates the median intensity of the HP-XY 'set' ratio, ranging from 0.035 (dark green) to 4.0 (dark red). The main display area shows a grid of data points, with some points highlighted in red and others in green. The grid is labeled with "1-A", "1-B", "1-C", "1-D", "2-C", and "2-D".

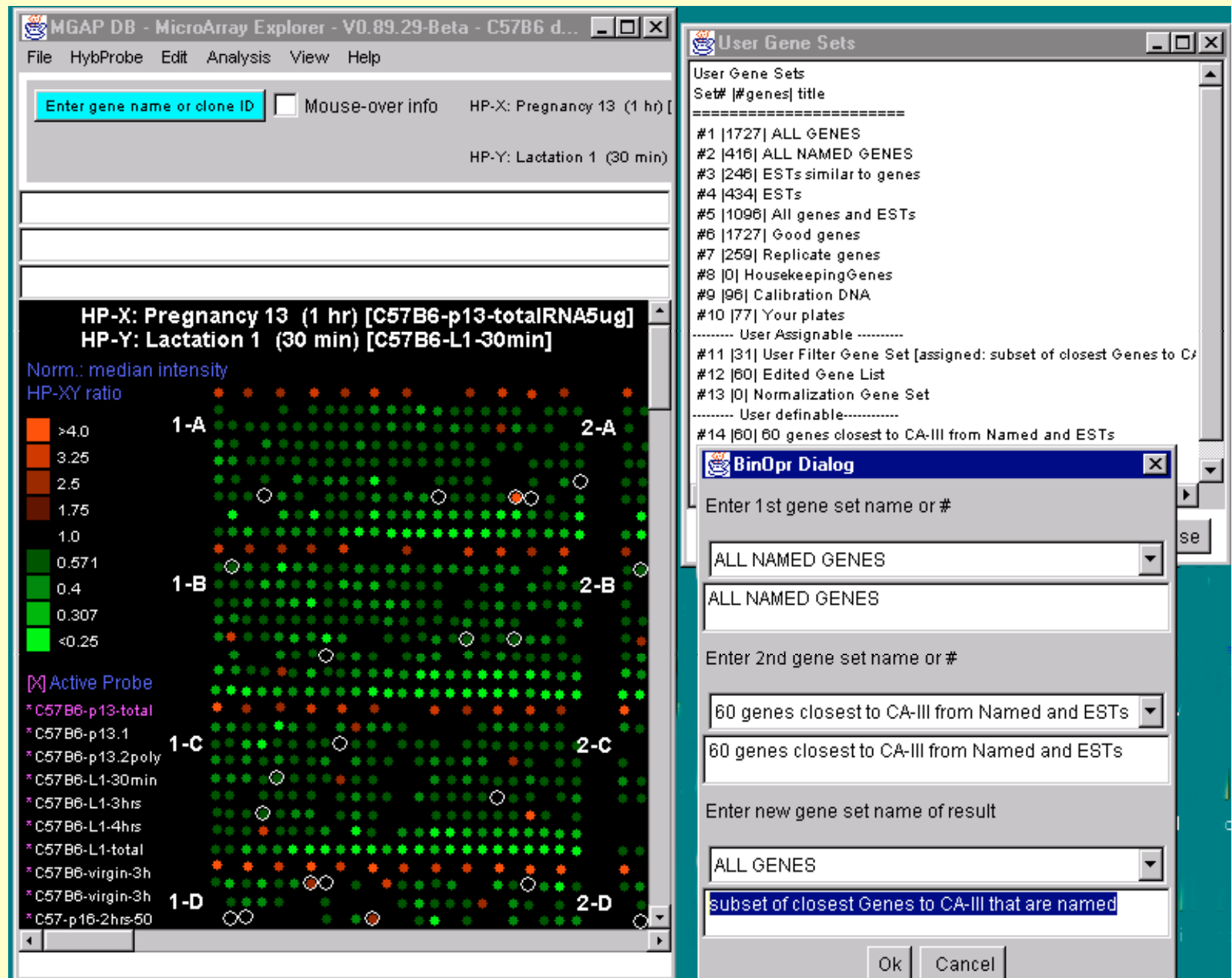
At the bottom left, there is a list of "Active Probe" entries, including "C57B6-virgin-3", "C57B6-p13-tota", "C57B6-p13.1", "C57B6-p13.2pol", "C57-p16-2hrs-5", "C57B6-L1-30min", "C57B6-L1-3hrs", "C57B6-L1-4hrs", "C57B6-L1-total", and "C57B6-L3-1hr".

On the right side, there is a "Preference sliders" window. It contains a section titled "State scrollers" with several sliders and their corresponding values: Intensity I1 (0.035), Intensity I2 (313.554), Ratio R1 (0.35), Ratio R2 (3.0), p-Value (0.01), and Spot CV (0.145).

## II.6a Gene Set Operations Help Manage Data and Search Results

- All gene sets are named with a directory of existing sets
- Set operations (AND, OR, DIFFERENCE) may be used to create new derived sets
- Special sets:
  1. Filtered genes set holds genes passing the data filter
  2. Edited Gene List holds results of clustering or editing
  3. Normalization set may be used as normalization method
  4. User data filter set may be used as a data filter
- Sets are saved when the session is saved, restored when MAExplorer is restarted

# II.6b Gene Set Operations - e.g. 'AND' of Two Sets



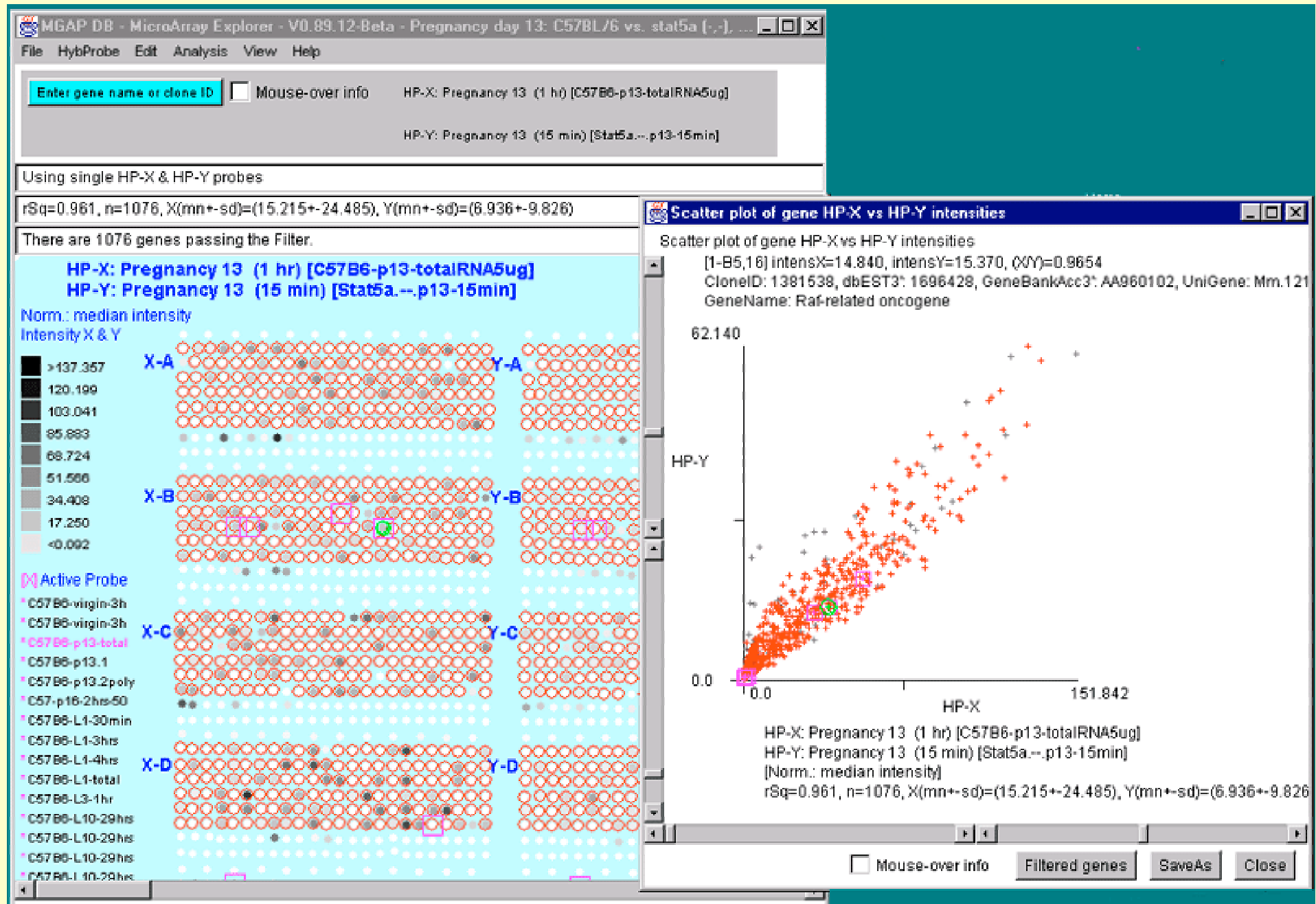


## II.7 Summary of Types of Plots

- Plots allow visualization and direct manipulation of gene data
- 1. Pseudo array image - intensity, ratio (X/Y)
- 2. Zoomable scatter plots - X vs Y, Cy3 vs Cy5, duplicate spots
- 3. Histograms - ratio and intensity
- 4. Expression profiles - individual genes and overlay plots
- 5. Silhouette plots - similarity clusters, K-means clustering
- 6. Hierarchical clustering - clustergram, dendrogram

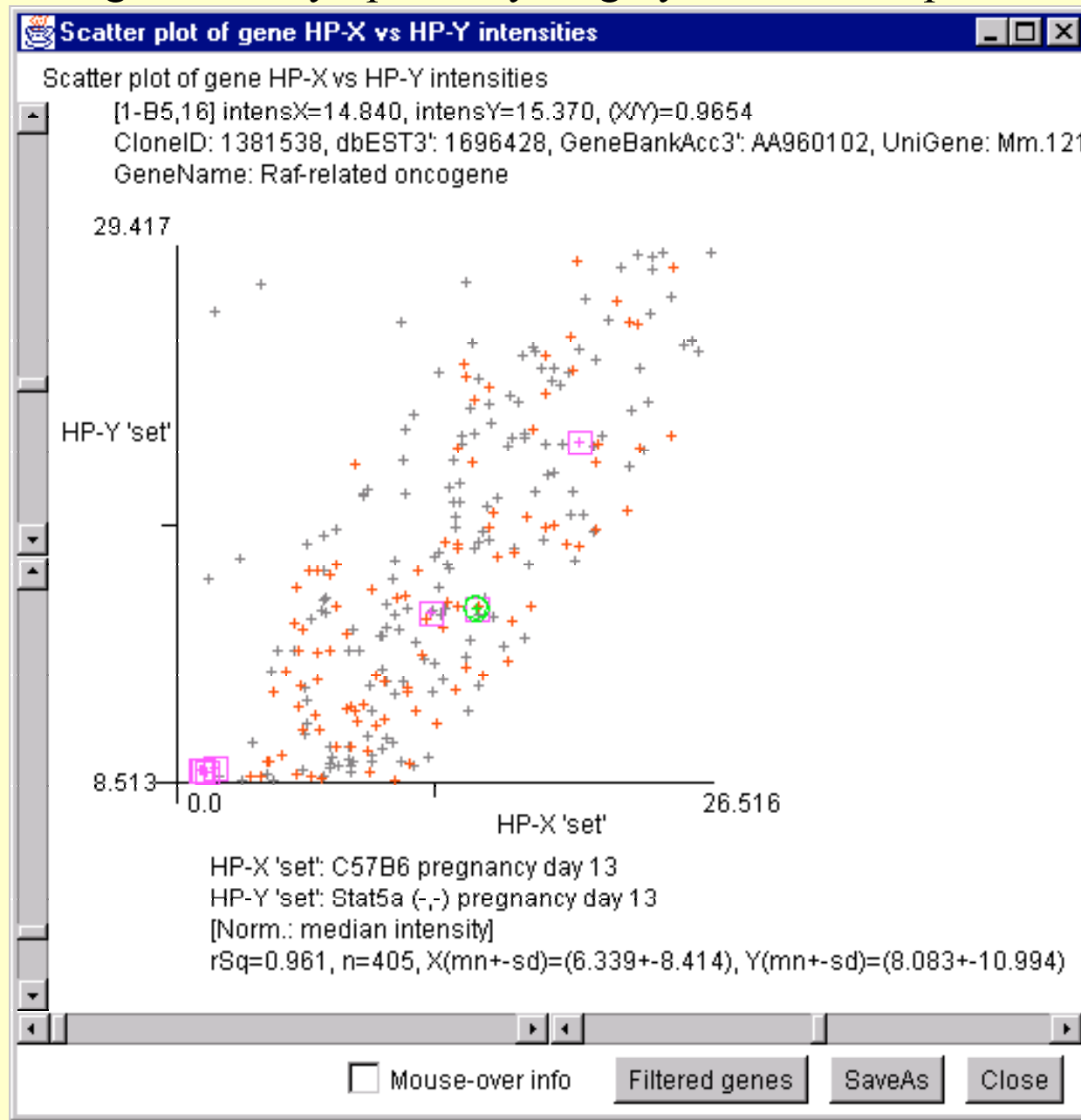
# II.8a Scatter Plots of Two Conditions

- X-Y scatter plot of two 13-day pregnancy samples: C57B6 vs Stat5a (-,-) [MGAP]

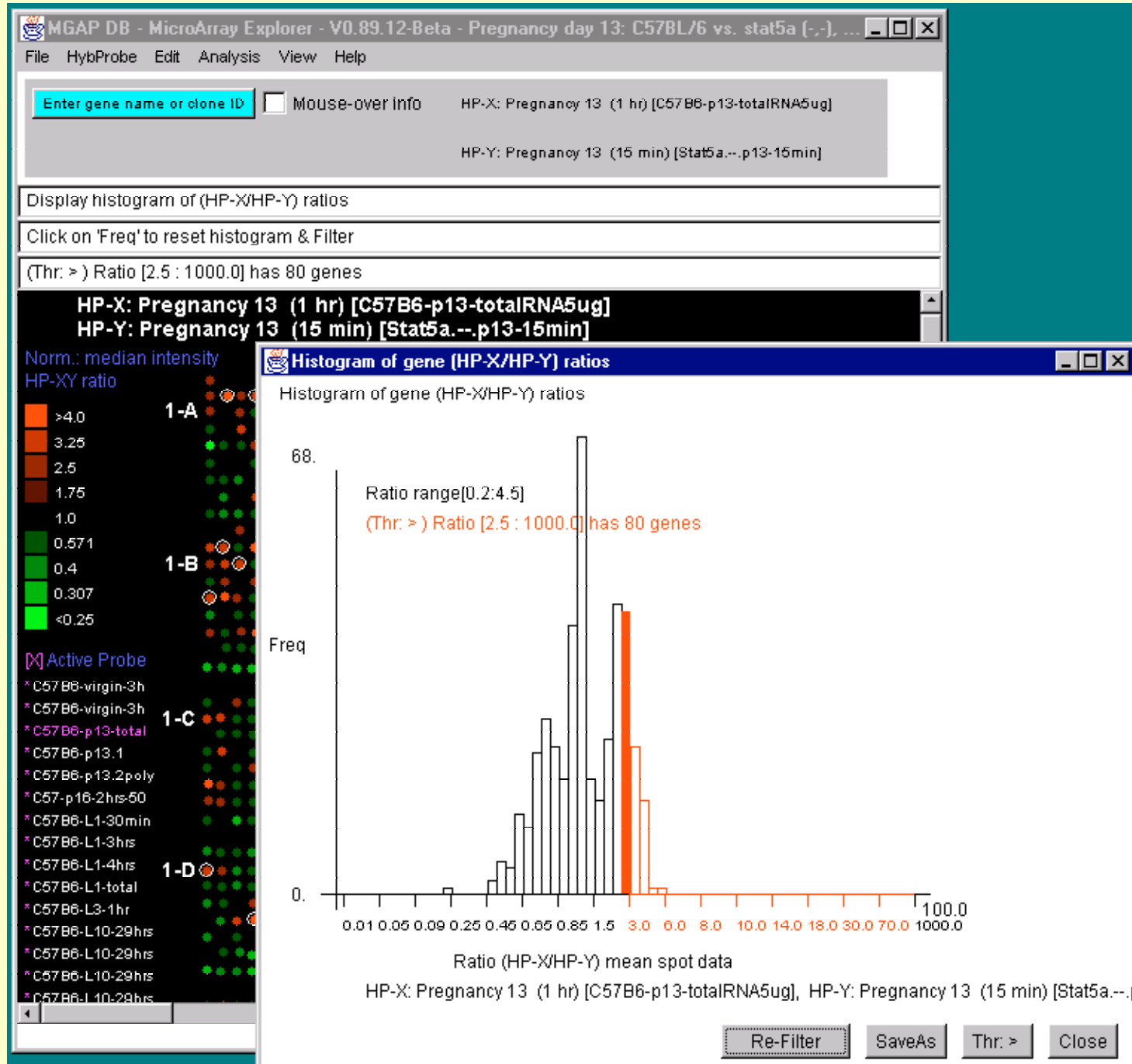


## II.8b Zoom X-Y Scatter Plot by Scrollers

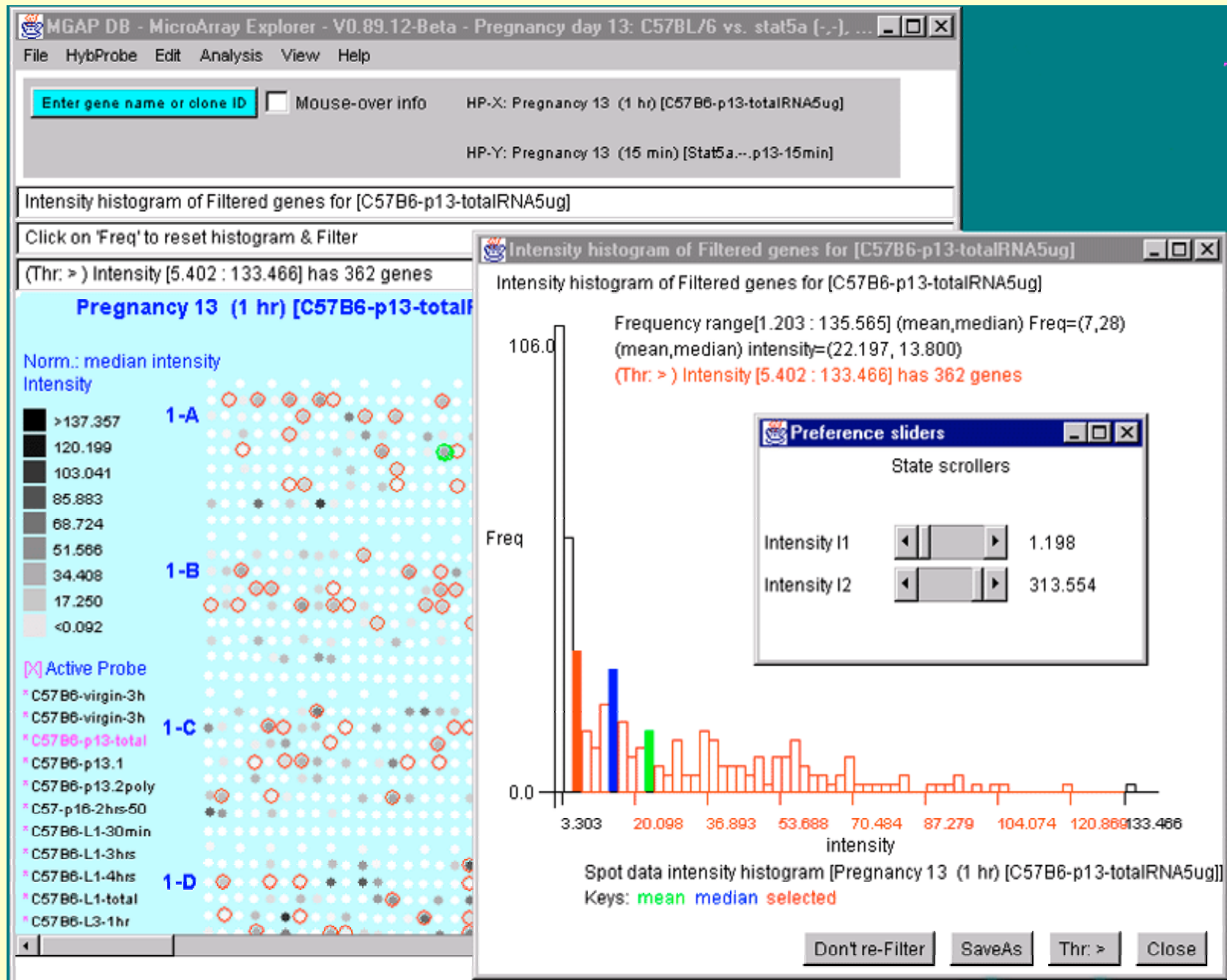
- Zoomed-in on Raf-related oncogene (green circle) using scrollbars
- Genes not passing Filter may optionally be grayed out in the plot



# II.9a Filter Genes by X/Y Ratio-Histogram Bin(s)



## II.9b Filter Genes by Intensity-Histogram Bin(s)



## II.10 Types of Reports

- Data reported as:
  1. Web-accessible scrollable dynamic spreadsheets or
  2. tab-delimited text exportable to Excel
- Gene set reports - linked to UniGene, GenBank, mAdb, etc.
- Array sample reports - linked to histology and model Web pages
- Pop-up Web browser on specific data from dynamic reports or plots

# II.11a Scrollable Dynamic Gene Reports - mAdb

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-), ...

File HybProbe Edit Analysis

Enter gene name or clone ID

GENE REPORT - Filtered genes with 50 Highest ratios HP-X[C57B6 pregnancy day 13] / HP-Y[Stat5a (-,-) pregnancy day 13]

GENE REPORT - Filtered genes with 50 Highest ratios HP-X[C57B6 pregnancy day 13] / HP-Y[Stat5a (-,-) pregnancy day 13]

F1 1382272

	Grid-Coord	Ratio HP-X/HP-Y	Clone-ID	Gene-Name	Plate-G,R,C	mAdb CloneDB
1	[1-G6,21]	1.9088	1382272	Mus musculus Msx-int	plate[10,G,9]	1382272
2	[1-B4,14]	1.8634	1248264	S100 calcium-binding	plate[B,B,2]	1248264

There are 405 genes passing t

HP-X: C57B6 pregna  
HP-Y: Stat5a (-,-) pr

Norm.: median intensity  
HP-XY 'set' ratio

>4.0  
3.25  
2.5  
1.75  
1.0  
0.571  
0.4  
0.307  
<0.25

1-A  
1-B  
1-C  
1-D

[X] Active Probe  
\* C57B6-p13-total  
\* C57B6-p13.1  
\* C57B6-p13.2poly  
\* Stat5a--p13-1  
\* Stat5a--p13-1  
\* Stat5a--p13-1  
\* Stat5a--p13-3  
\* Stat5a--p13-3  
\* C57B6-virgin-3h  
\* C57B6-virgin-3h  
\* C57-p16-2hrs-60

Clone Report - Netscape

File Edit View Go Communicator Help

Bookmarks Location: [http://nciarray.nci.nih.gov/cgi-bin/clone\\_report.cgi?CRITERIA=clone&PARAMETER=IMAGE:1382272](http://nciarray.nci.nih.gov/cgi-bin/clone_report.cgi?CRITERIA=clone&PARAMETER=IMAGE:1382272)

Back Forward Reload Home Search Netscape Print Security Shop Stop

Division of Clinical Sciences NCI  
CIT Center for Information Technology

## NCI *mAdb* Clone Report

Clone [IMAGE:1382272](#)

Library Source Soares\_mammary\_gland\_NMLMG

Sequence Verification Unknown

3' Sequence [AI462206](#) BLAST Results: [NT](#) [NR](#)

5' Sequence [AA798388](#) BLAST Results: [NT](#) [NR](#)

3' & 5' UG Title Msx-interacting-zinc finger

3' & 5' UG Cluster [tp Mm.6370](#) NCBI's [LocusLink](#) Stanford's [S.O.U.R.C.E.](#)

3' & 5' UG Gene Miz1

3' & 5' UG RefSeq [NM 008602](#)

Document: Done



# II.11b Scrollable Dynamic Gene Report - UniGene

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-), ...

File HybProbe Edit Analysis View Help

☐ Mouse-over info

HP-X: C57B6 pregnancy day 13  
HP-Y: Stat5a (-,-) pregnancy day 13

[1-D4,1] HP-XY 'sets':  $mn(X,Y)=(1.525,2.787)$   $mnX/mnY=0.547$   $SD(X,Y)=(0.149,0.173)$   $CV(X,Y)=(0.098,0.062)$   $n(X,Y)=...$

CloneID: 1248016, dbEST3: 227773

GeneName: Cysteine rich protein

HP-X: C57B6 pregnancy day 13  
HP-Y: Stat5a (-,-) pregnancy day 13

Norm.: median intensity  
HP-XY 'set' ratio

>4.0

3.25

2.5

1.75

1.0

0.571

0.4

0.307

<0.25

1-A

1-B

1-C

1-D

☒ Active Probe

\* C57B6-p13-total

\* C57B6-p13.1

\* C57B6-p13.2poly

\* Stat5a...p13-1

\* Stat5a...p13-1

\* Stat5a...p13-1

\* Stat5a...p13-3

\* Stat5a...p13-3

\* C57B6-virgin-3h

\* C57B6-virgin-3h

\* C57-p16-2hrs-50

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CIT

NCI

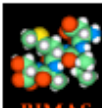
Center for Information Technology

NCIArray [NCBI](#) Mm [UniGene](#) Query Results

Local Mm Database updated to build #86 on Feb 12, 2001

2 records satisfy the query clone like "IMAGE:1248016" for Organism Mm

Clone	GB Accession	UniGene	Description	Symbol
IMAGE:1248016	<a href="#">AA959891</a>	<a href="#">Mm.10919</a>	cysteine rich protein	<a href="#">Csrp</a>
IMAGE:1248016	<a href="#">AI461843</a>	<a href="#">Mm.10919</a>	cysteine rich protein	<a href="#">Csrp</a>

 NIH Bioinformatics support provided by [BIMAS/CBEL/CIT](#).  
We can be contacted by [email](#).



# II.12a Sample Information Array Reports

- Details are available on all hybridized array samples

All Sample Hybridizations in the Database						
All Sample Hybridizations in the Database						
A21	C57B6 P13 total RNA 5ug					
	Membrane_ID	Beta	Source	Strain	Stage	Probe
14	C57B6 L1 30min	-	control	C57B6	Lactation 1	mammary gland
15	C57B6 L1 3hrs	-	control	C57B6	Lactation 1	mammary gland
16	C57B6 L1 4hrs	-	control	C57B6	Lactation 1	mammary gland
17	C57B6 L1 total RNA	-	control	C57B6	Lactation 1	mammary gland
18	C57B6 L3 1hr	-	control	C57B6	Lactation 3	mammary gland
19	C57B6 P13.1 poly(A)	-	control	C57B6	Pregnancy 13	mammary gland
20	C57B6 P13.2 poly(A)	-	control	C57B6	Pregnancy 13	mammary gland
21	C57B6 P13 total RNA	-	control	C57B6	Pregnancy 13	mammary gland
22	C57B6 virgin 3 hours	-	control	C57B6	Virgin 10 weeks old	mammary gland

Close

## II.12b Correlation Report of All Samples

- Sample vs Sample correlation coefficient report for *current set* of **Filtered** genes

HP vs. HP correlation coefficients table, Pregnancy 13 days: C57BL/6 vs. stat5a (-,-), 8 probes

HP vs. HP correlation coefficients table, Pregnancy 13 days: C57BL/6 vs. stat5a (-,-), 8 probes

D2 rSq=0.982, n=405, HP:2(mn+-sd)=(1+-0), HP:3(mn+-sd)=(1+-1)

		C57B6-p13-totalRNAf	C57B6-p13.1	C57B6-p13.2poly-A	Stat5a...p13-15min	Stat5a...p13-15min2
1	C57B6-p13-totalRNAf	-	rSq=0.715, n=405, Hf	rSq=0.729, n=405, Hf	rSq=0.953, n=405, Hf	rSq=0.958, n=405, Hf
2	C57B6-p13.1	-	-	rSq=0.982, n=405, Hf	rSq=0.756, n=405, Hf	rSq=0.757, n=405, Hf
3	C57B6-p13.2poly-A	-	-	-	rSq=0.772, n=405, Hf	rSq=0.773, n=405, Hf
4	Stat5a...p13-15min	-	-	-	-	rSq=0.997, n=405, Hf
5	Stat5a...p13-15min2	-	-	-	-	-
6	Stat5a...p13-1hr2	-	-	-	-	-
7	Stat5a...p13-30min	-	-	-	-	-
8	Stat5a...p13-30min2	-	-	-	-	-
9	-	-	-	-	-	-

Close

# II.13 Tab-Delimited Reports Exportable to Excel

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-), ...

File HybProbe Edit Analysis View Help

Enter gene name or clone ID ☐ Mouse-over info HP-X: C57B6 pregnancy day 13

HP-Y: Stat5a (-,-) pregnancy day 13

Genes with highest HP-X/HP-Y ratios

There are 405 genes passing the Filter.

**HP-X: C57B6 pregnancy day 13**  
**HP-Y: Stat5a (-,-) pregnancy day 13**

Norm.: median intensity  
 HP-XY 'set' ratio

☐ Active Probe  
 \* C57B6-p13-total  
 \* C57B6-p13.1  
 \* C57B6-p13.2poly  
 \* Stat5a-,-p13-1  
 \* Stat5a-,-p13-1  
 \* Stat5a-,-p13-1  
 \* Stat5a-,-p13-3  
 \* Stat5a-,-p13-3  
 \* C57B6-virgin-3h  
 \* C57B6-virgin-3h  
 \* C57-p16-2hrs-50

1-A  
 1-B  
 1-C  
 1-D

>4.0  
 3.25  
 2.5  
 1.75  
 1.0  
 0.571  
 0.4  
 0.307  
 <0.25

**GENE REPORT - Filtered genes with 50 Highest ratios HP-X[C57B6 preg...]**

GENE REPORT - Filtered genes with 50 Highest ratios HP-X[C57B6 pregnancy day 13] / HP-Y[Stat5a

Grid-Coord	Ratio HP-X/HP-Y	Clone-ID	Gene-Name	Plate-G,R,C	mAdb Cl
[1-G6,21]	1.9088	1382272	Mus musculus Msx-interacting-zinc finger protein 1 (Miz1) mRNA, comp		
[1-B4,14]	1.8634	1248264	S100 calcium-binding protein A4	plate[6,B,2]	1248264
[1-A3,17]	1.8456	1248170	Mouse mRNA for SDF2, complete cds	plate[4,A,5]	1248170
[1-H4,15]	1.8449	1248272	ADRENODOXIN PRECURSOR	plate[6,H,3]	1248272
[1-D5,3]	1.8256	1248351	Abl-interactor 1	plate[7,D,3]	1248351 1248351 AI463372
[1-F7,7]	1.8118	1382525	Acetyl coenzyme A dehydrogenase, medium chain	plate[11,F,7]	
[1-C2,19]	1.7997	1247627	Mus musculus mRNA for osteomodulin, complete cds	plate[2,C,2]	
[1-A3,6]	1.7677	1247777	Mus musculus metalloprotease/disintegrin/cysteine rich protein precurs		
[1-B6,7]	1.7562	1381654	TROPOMYOSIN 5, CYTOSKELETAL TYPE	plate[9,B,7]	
[1-B6,9]	1.7499	1381703	B-cell translocation gene 2, anti-proliferative	plate[9,B,9]	
[1-A5,23]	1.7377	1248527	Mus musculus ubiquitin-conjugating enzyme HR6A mRNA, complete c		
[1-C3,10]	1.7316	1247708	Ephrin A1	plate[3,C,10]	1247708 1247708 AA959770
[1-D3,5]	1.7249	1247564	Erythrocyte protein band 7.2	plate[3,D,5]	1247564 1247564
[1-C6,2]	1.7190	1381920	Mus musculus mRNA for NEFA protein, complete cds		plate[9,C,2]
[1-D7,16]	1.7081	1382671	Mouse MA-3 (apoptosis-related gene) mRNA, complete cds		plate[12,D,7]
[1-H3,12]	1.7073	1248169	Histocompatibility 2, T region locus 22	plate[3,H,12]	1248169
[1-H4,20]	1.7039	1248345	Mus musculus alpha-methylacyl-CoA racemase mRNA, complete cds		
[1-D2,14]	1.6611	1247820	Tight junction protein 1	plate[2,D,2]	1247820 1247820
[1-A2,22]	1.6598	1247817	Mus musculus ras-related protein (rab18) mRNA, complete cds		
[1-D4,6]	1.6528	1248184	Mus musculus bromodomain-containing protein BP75 mRNA, complet		
[1-C5,5]	1.6274	1248278	HISTONE H3.3	plate[7,C,5]	1248278 1248278 AI463306

SaveAs Close

## **II.14 [Undergoing *Beta*-testing]**

### **Data Conversion for MAExplorer: Cvt2Mae**

- Cvt2Mae reads and converts a variety of array data to MAExplorer format:
  1. commercial arrays (Incyte, Affymetrix, etc.)
  2. user-defined academic arrays
- Cvt2Mae is undergoing testing and will be made available for download through the MAExplorer Web site

# II.15a Initial State of Cvt2Mae Program

**Cvt2Mae: convert array data to MAExplorer files - Version: 06-21-2001**

1. Select Chipset: -- select a chip layout --

1.1 (opt.) Select Quant. software used: [NONE] pick array data ()

2. Select Input Data Files: Browse input file name

2.1 Samples to use '<<file>> sample name' Remove sample Rename sample

Vendor	
Layout name	
Species	
Spots/microarray	

3. Select Project Output Folder: --Select Output Folder--

Project output directory: D:\Java-Work Shop20\JWS\intel-win32\bin\

MAExplorer startup File:

4. Edit and Run Run Edit Layout Assign GIPO fields Assign Quant fields Abort

☐ Expert assign-mode

Status:

## II.15b Select a Chip Array-Layout

Cyt2Mae: convert array data to MAExplorer files - Version: 06-19-2001-am.1

1. Select Chipset: Incyte - Human

1.1 (opt.) Select Quant. software used: [Incyte] GemTool (G)

2. Select Input Data Files:

2.1 Samples to use '<<file>> sample name'

Vendor: Incyte

Layout name: Incyte - Human

Species: Human

Spots/microarray: 0

3. Select Project Output Folder: Use input folder for output files

Project output directory: D:\Java-WorkShop20\JWS\intel-win32\bin\

MAExplorer startup File:

4. Edit and Run

Run Edit Layout Assign GPO fields Assign Quant fields Abort

☐ Expert assign-mode

Status:

# II.16c Select Input Files with Input-Browser

Cvt2Mae: convert array data to MAExplorer files - Version: 06-19-2001-am.1

1. Select Chipset:

1.1 (opt.) Select Quant. software used:

2. Select Input Data Files:

4142.cgi  
4143.cgi  
4144.cgi

2.1 Samples to use '<<file>> sample name'

<<F:\Temp\LAdat\LA-6Hybes\4142.cgi>> 4142.cgi  
<<F:\Temp\LAdat\LA-6Hybes\4143.cgi>> 4143.cgi  
<<F:\Temp\LAdat\LA-6Hybes\4144.cgi>> 4144.cgi

Vendor	Layout name	Species	Spots/microarray
Inc	Inc	Hu	72

3. Select Project Output Folder:

Project output directory:   
MAExplorer startup File:

4. Edit and Run

☐ Expert assign-mode

Status: There are 7275 rows of data in file [4144.cgi]

Select the next input file to convert

Look in:

- 4142.cgi
- 4143.cgi
- 4144.cgi
- 4145.cgi**
- 4146.cgi
- 4147.cgi

File name:

Files of type:

# II.17d Optional Edit Layout - Defining Geometry

Cvt2Mae: convert array data to MAExplorer files - Version: 06-19-2001-am.1

1. Select Chipset: **Incyte - Human**

1.1 (opt.) Select Quant. software used: **[Incyte] GemTool (GIPO: GRC)**

2. Select Input Data Files:

4142.cgi  
4143.cgi  
4144.cgi  
4145.cgi

2.1 Samples to use '<<file>>' sample

<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414

3. Select Project Output Folder:

Project output di  
MAExplorer star

4. Edit and Run

**Run** **Edit Layout** **Assign GIPO fields** **Assign Quant fields** **Abort**

☐ Expert assign-mode

Status: **There are 7275 rows of data in file [4145.cgi]**

**Edit MAExplorer project**

[1] Grid Geometry Data

Number of duplicated spot Fields in array	1
Number of Grids per Field	5
Number of spots per Grid Row	33
Number of spots per Grid Column	45
Specify array layout by Grid-geometry or by # spots/array	<input checked="" type="checkbox"/> Use # spots (below), else grid-geometry (above)
Maximum number of spots in array	7275

If you specify the array layout by Grid-geometry, then enter (#Fields, #Grids, #Grid-rows, #Grid-cols). If you specify the layout by the maximum number of spots in the array, it will estimate a pseudo-layout that the spots will fit on the this array for visualization purposes. It does not correspond to the actual array layout which you do not have to enter.

<Back Next> Done



# II.17e Edit Layout - Specify Input File Rows

Cvt2Mae: convert array data to MAExplorer files - Version: 06-19-2001-am.1

1. Select Chipset: Incyte - Human

1.1 (opt.) Select Quant. software used: [Incyte] GemTool (GIPO:GRC)

2. Select Input Data Files:

4142.cgi  
4143.cgi  
4144.cgi  
4145.cgi

2.1 Samples to use '<<file>>' sample

<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414

3. Select Project Output Folder:

Project output di  
MAExplorer star

4. Edit and Run

Run Edit Layout Assign GIPO fields Assign Quant fields Abort

☐ Expert assign-mode

Status: There are 7275 rows of data in file [4145.cgi]

**Edit MAExplorer project**

[2] Input file starting rows data

(Optional) Row containing list sample names	0
Row containing list of data field names	7
First row containing quantitative data	0
(Optional) Comment token	#
(Optional) Initial keyword for each data row	GEMID

Number of row that contains the names of the data fields in the file. Eg. grid, row, column, GeneBank ID, GeneName, Clone ID, etc. [Row #s start at row 1.]

<Back Next> Done

# II.17f Edit Layout - Intensity or Ratio Data

Cvt2Mae: convert array data to MAExplorer files - Version: 06-19-2001-am.1

1. Select Chipset: **Incyte - Human**

1.1 (opt.) Select Quant. software used: **[Incyte] GemTool (GIPO: GRC)**

2. Select Input Data Files:

4142.cgi  
4143.cgi  
4144.cgi  
4145.cgi

2.1 Samples to use '<<file>> sample':

<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414  
<<F:\Temp\LAdat\LA-6Hybes\414

3. Select Project Output Folder:

Project output di  
MAExplorer star

**Edit MAExplorer project**

[4] Ratio fluorescence data

Ratio (i.e. Cy3,Cy5) or Intensity Data ☒ Use Ratio else Intensity data

If Ratio data, use (Cy5/Cy3) else (Cy3/Cy5) ☐ Use (Cy5/Cy3) else (Cy3/Cy5)

Fluorescent dye for intensity 1 **Cy3**

Fluorescent dye for intensity 2 **Cy5**

Data for MAExplorer is either ratio data such as Cy3/Cy5, or intensity data such as P33, etc.

<Back **Next>** Done

4. Edit and Run **Run** **Edit Layout** **Assign GIPO fields** **Assign Quant fields** **Abort**

☐ Expert assign-mode

Status: **There are 7275 rows of data in file [4145.cgi]**

# II.17g Specify Output Folder for Converted Data

Cvt2Mae: convert array data to MAEExplorer files - Version: 06-19-2001-am.1

1. Select Chipset: Incyte - Human

1.1 (opt.) Select Quant. software used: [Incyte] GemTool (GIPO:GRC)

2. Select Input Data Files: Browse input file name

4142.cgi  
4143.cgi  
4144.cgi  
4145.cgi

2.1 Samples to use '<<file>> sample name'

<<F:\Temp\LAdat\LA-6Hybes\4142.cgi>>  
<<F:\Temp\LAdat\LA-6Hybes\4143.cgi>>  
<<F:\Temp\LAdat\LA-6Hybes\4144.cgi>>  
<<F:\Temp\LAdat\LA-6Hybes\4145.cgi>>

Select the project directory to save data

Save in: junk

Cache  
Config  
MAE  
Quant  
Report  
State

MAErr.log

File name: Select project directory - then press 'Save'

Save as type: All Files (\*.\*)

Save  
Cancel

3. Select Project Output Folder: Create New project folder

Project output directory: F:\Temp\LAdat\LA-6Hybes\

MAEExplorer startup File: F:\Temp\LAdat\LA-6Hybes\MAE\Start.mae

4. Edit and Run

Run Edit Layout Assign GIPO fields Assign Quant fields Abort

☐ Expert assign-mode

Status: There are 7275 rows of data in file [4145.cgi]

# II.17h Optionally Assign GIPO Fields

Cvt2Mae: convert array data to MAExplorer files - Version: 06-19-2001-am.1

1. Select a dataset: **Incyte - Human**

1.1 Assign user fields to GIPO fields

Location	Location
Plate	PlateID
Plate row	PlateRow
Plate col	PlateCol
field	<not used>
grid	<not used>
grid row	<not used>
grid col	<not used>
NAME_GRC	<not used>
QualCheck	<not used>
Clone ID	<not used>
GeneName	GeneName
GenBankAcc	<not used>

2. Select input file name: **Browse input file name**

Remove sample | Rename sample

42.cgi  
43.cgi  
44.cgi  
45.cgi

Vendor: **Incyte**

Layout name: **Incyte - Human**

Species: **Human**

Probes/microarray: **7275**

3. Select project output folder

Create New project folder

Project folder: **F:\Temp\junk\**

MAExplorer file: **F:\Temp\junk\MAE\Start.mae**

4. Edit and Run

**Run** | **Edit Layout** | **Assign GIPO fields** | **Assign Quant fields** | **Abort**

☐ Expert assign-mode

Status: \_\_\_\_\_

# II.17i Optionally Assign Quantified Data Fields

Cvt2Mae: convert array data to MAExplorer files - Version: 06-19-2001-am.1

1. Select Chipset: **Incyte - Human**

1.1 (opt.) Select Quant. software used: **[Incyte] GemTool (GIPO:GRC)**

2. Select Input Data Files:

4142.cgi  
4143.cgi  
4144.cgi  
4145.cgi

2.1 Samples to use '<<file>>' samples

<<F:\Temp\LAdat\LA-6Hybes\4142\4142.cgi>>  
<<F:\Temp\LAdat\LA-6Hybes\4143\4143.cgi>>  
<<F:\Temp\LAdat\LA-6Hybes\4144\4144.cgi>>  
<<F:\Temp\LAdat\LA-6Hybes\4145\4145.cgi>>

3. Select Project Output Folder:

Project output folder: **MAExplorer si**

4. Edit and Run **Run**

**Assign user fields to Quantitation fields**

Location	Location
X	<not used>
Y	<not used>
field	<not used>
grid	<not used>
grid col	<not used>
grid row	<not used>
NAME_GRC	<not used>
RawIntensity	<not used>
RawIntensity1	P1Signal
RawIntensity2	P2Signal
Background	<not used>
Background1	P1S/B
Background2	<not used>
	P1Area%
	P2BalancedSig
	P2Signal
	P2S/B
	P2Area%
	Probe1
	P1Description
	Probe2

**Assign Quant fields**

**Abort**

Status: **Code**

# II.18a Converted Incyte files Ready to Analyze

**Cvt2Mae: convert array data to MAExplorer files - Version: 06-21-2001**

1. Select Chipset: Incyte - Human

1.1 (opt.) Select Quant. software used: [Incyte] GemTool (GIPO: GRC)

2. Select Input Data Files: Browse input file name

4142.cgi  
4143.cgi  
4144.cgi  
4145.cgi

2.1 Samples to use '<<file>> sample name' Remove sample Rename sample

<<F:\Temp\Adata\LA-6Hybes\4142.cgi>> 4142.cgi  
<<F:\Temp\Adata\LA-6Hybes\4143.cgi>> 4143.cgi  
<<F:\Temp\Adata\LA-6Hybes\4144.cgi>> 4144.cgi  
<<F:\Temp\Adata\LA-6Hybes\4145.cgi>> 4145.cgi

Vendor	Incyte
Layout name	Incyte - Human
Species	Human
Spots/microarray	7275

3. Select Project Output Folder: Create New project folder

Project output directory: F:\Temp\junk\

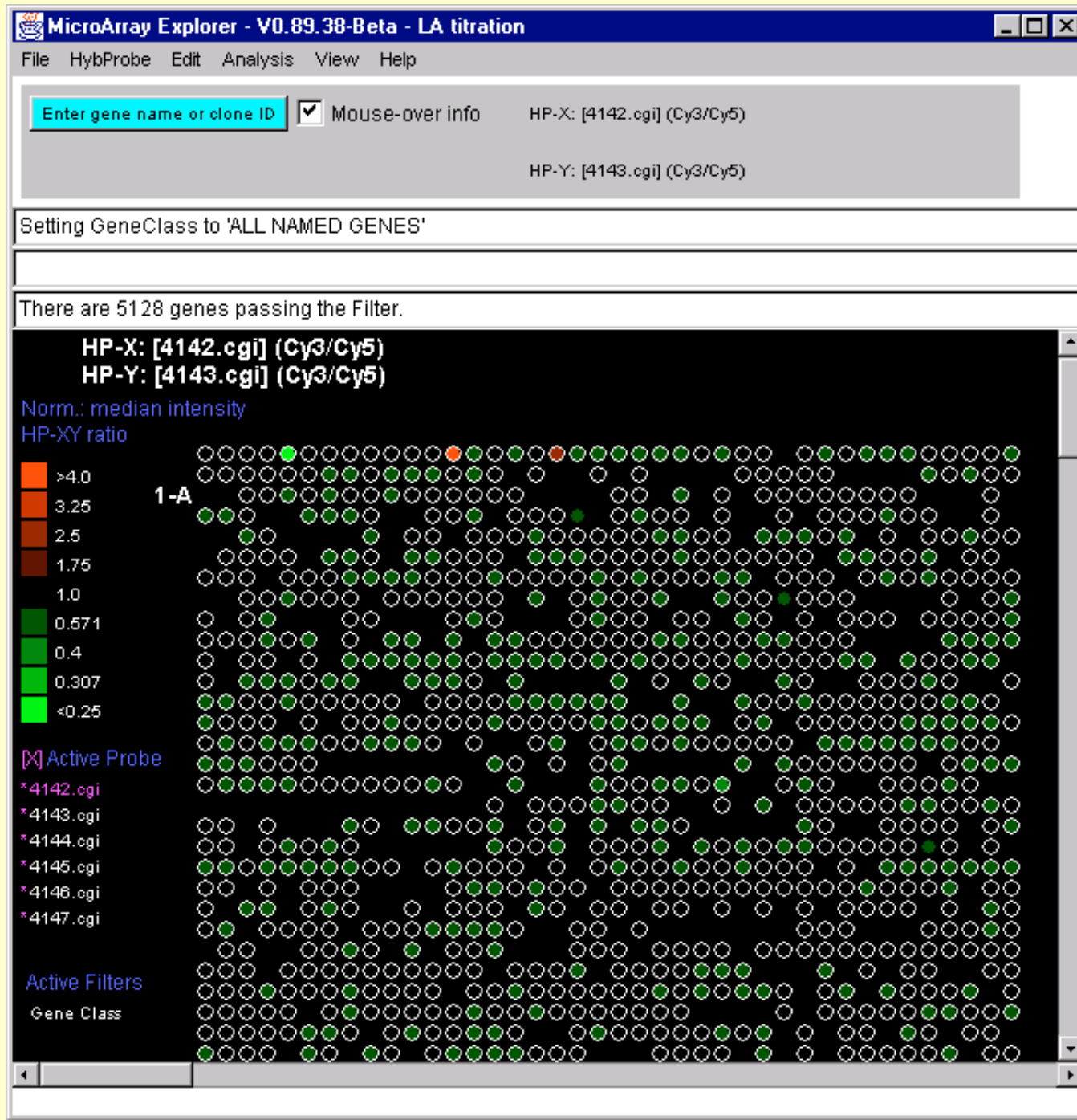
MAExplorer startup File: F:\Temp\junk\MAE\Start.mae

4. Edit and Run Run Edit Layout Assign GIPO fields Assign Quant fields Done

☐ Expert assign-mode

Status: ====> Finished writing out data files. Press 'Done' to exit  
To start MAExplorer, go to project folder & click on Start.mae.

# II.18b Incyte Data from Cvt2Mae Conversion



# II.19a Converted Affymetrix files for Analysis

**Cvt2Mae: convert array data to MAExplorer files - Version: 07-17-2001** [-] [x]

Enter data for steps 1, 2, and 3. Then press 'Run' to convert your data to MAExplorer format.

1. Select Chipset: Affymetrix - Human

1.1 (opt.) Select Quant. software used: [NONE] pick array data ()

2. Select Input Data Files: Browse input file name

U937-Affymetrix-2subclones.txt

2.1 Samples to use '<<file>> sample name' Remove sample Rename sample

<<F:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel10A-1-U95A]
<<F:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel10B-1-U95A]
<<F:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel17A-1-U95A]
<<F:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel17B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - Human
Species	Human
Spots/microarray	12630

3. Select Project Output Folder: Create New project folder

Project output folder: F:\Temp\junk\

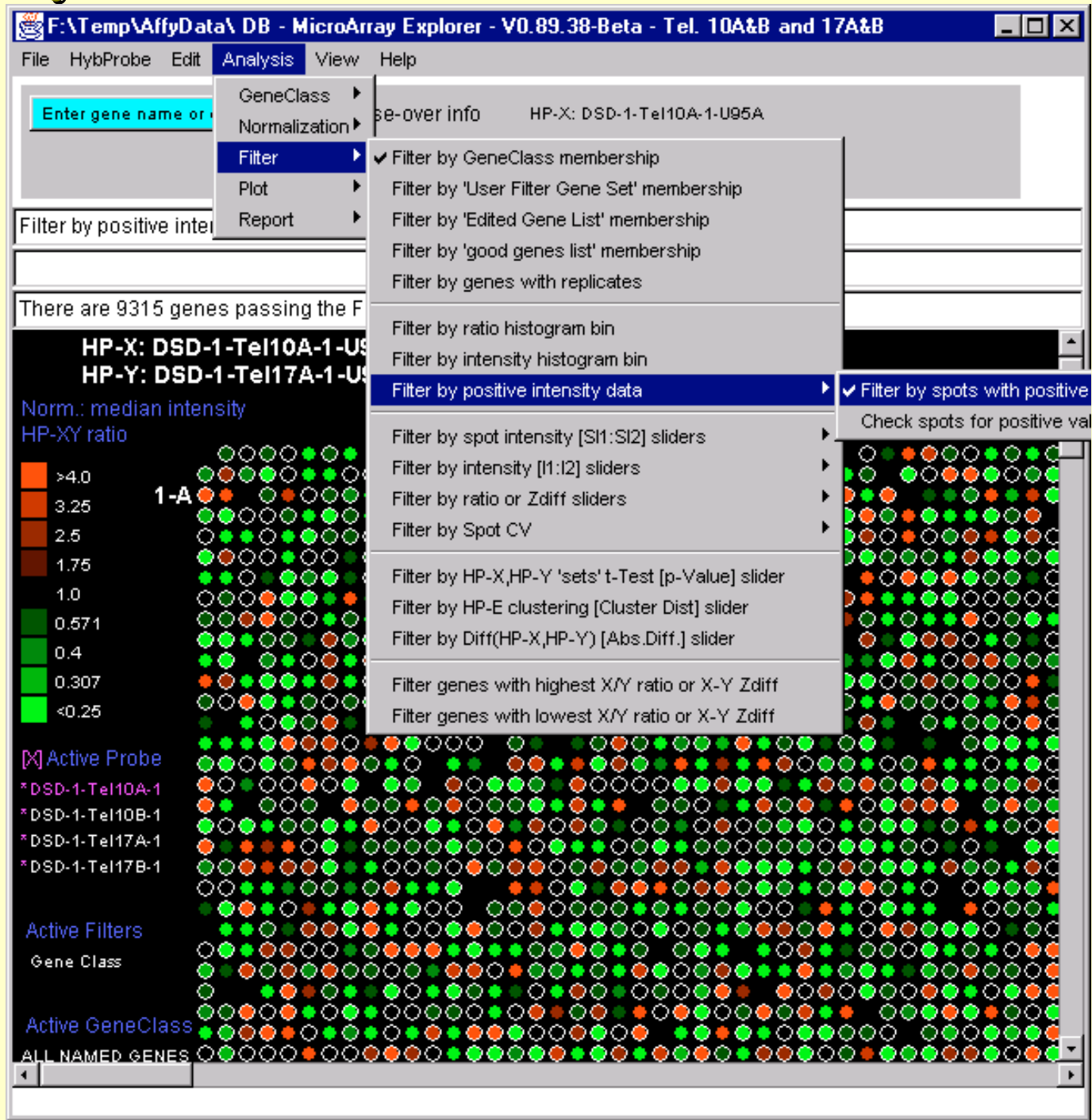
MAExplorer startup File: F:\Temp\junk\MAE\Start.mae

4. Edit and Run Run Edit Layout Assign GPO fields Assign Quant fields Save Layout ☐ Expert assign-mode Done

Status: ====> Finished writing out data files. Press 'Done' to exit  
To start MAExplorer, go to project folder & click on Start.mae.



# II.19b Affymetrix Data from Cvt2Mae Conversion



## II.20 Using MAExplorer with mAdb Data

- The **NCI/CIT mAdb Web microarray database server** is an array data repository and analysis facility for microarrays created in conjunction with the NCI-ATC facility (<http://nciarray.nci.nih.gov/>)
- It can create a set of data files, downloaded as a Zip file from the mAdb, in a ready-to-use format compatible with MAExplorer
- **Section III** describes the procedure for **downloading MAExplorer**. You should periodically check the MAExplorer Web site to see if there is a major revision that you might want to download
- **Section IV** describes the procedure for **downloading a mAdb data set** and starting MAExplorer on that data.
- **Help desk for MAExplorer:** *mae@ncifcrf.gov*  
Peter Lemkin (301-846-5535)  
Greg Thornwall (301-846-5539)

# Summary

- MAExplorer is a flexible microarray data-mining tool running on the user's computer
- Uses direct-manipulation, data filtering, built-in graphics, statistics, clustering, gene and sample set operations
- Manages multiple samples, replicates, sets, expression profile lists where the state may be saved on the disk for later use
- Cvt2Mae data conversion tools allows use with common chips
- Plug-ins will allow extension with new analytic methods by users
- MAExplorer identified genes in preferentially expressed during lactation, *Nucleic Acids Res.* (2000) **28**:4452
- Freely available for download with documentation on Web site